MultiQC

A modular tool to aggregate results from bioinformatics analyses across many samples into a single report.

Report generated on 2022-04-23, 15:57 based on data in: `/home/khoidnyds/RNAseq_old/6.tophat2`

Welcome! Not sure where to start? Watch a tutorial video *(6:06)* don't show again

General Statistics

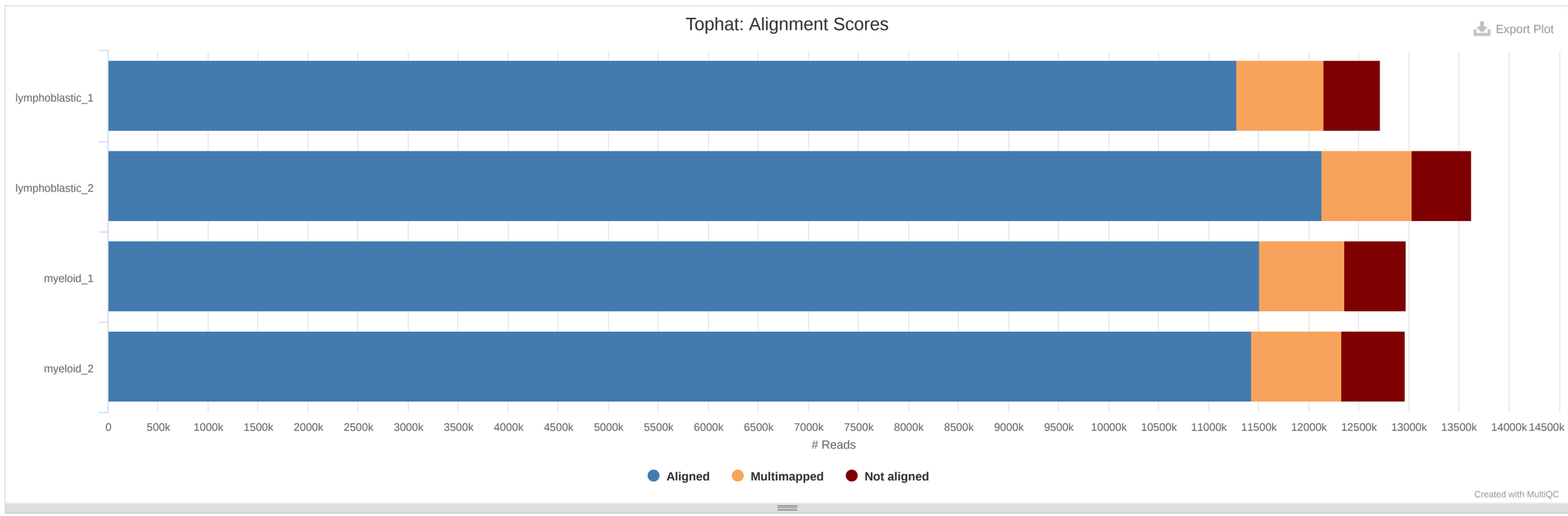
Copy table | Configure Columns | Plot | Showing 10/10 rows and 3/3 columns.

Sample Name	% Aligned	M Aligned	% Aligned
bowtie.left_kept_reads			83.9%
bowtie.left_kept_reads_seg1			35.0%
bowtie.left_kept_reads_seg2			50.4%
bowtie.left_kept_reads_seg3			54.1%
bowtie.left_kept_reads_seg4			53.0%
bowtie.left_kept_reads_seg5			29.1%
lymphoblastic_1	95.5%	11.3	
lymphoblastic_2	95.6%	12.1	
myeloid_1	95.2%	11.5	
myeloid_2	95.1%	11.4	

Tophat

Tophat is a fast splice junction mapper for RNA-Seq reads. It aligns RNA-Seq reads to mammalian-sized genomes. *DOI: 10.1186/gb-2013-14-4-r36; 10.1093/bioinformatics/btp120.*

Number of Reads | Percentages



Bowtie 2 / HiSAT2

Bowtie 2 and HISAT2 are fast and memory-efficient tools for aligning sequencing reads against a reference genome. Unfortunately both tools have identical log output by default, so it is impossible to distiguish which tool was used. . *DOI: 10.1038/nmeth.1923; 10.1038/nmeth.3317; 10.1038/s41587-019-0201-4.*

Single-end alignments

Help

This plot shows the number of reads aligning to the reference in different ways.

Number of Reads | Percentages